

Attorney Docket No. 21715/1010
U.S.S.N. 09/689,952
Filed October 12, 2000

Marked-up sheets showing changes made in the amendment:

1. Please replace the last paragraph on page 11 of the present specification with the following paragraph:

“Fig. 5 shows the predicted tryptic peptide masses of the ORF (SEQ ID NOs: 10-13) identified in the University of Oklahoma *S aureus* genomic database that closely matches the tryptic peptide profile of the polypeptide bound by 77ORF104.”

2. Please replace the last paragraph on page 45 of the present specification with the following paragraph:

“Comparison of the ORF of the *S. aureus* contig that encodes a tryptic peptide similar to that identified in the *S. aureus* phage 77 ORF 104 binding studies with all other sequences in the public domain databases revealed that the ORF is related to the Dnal protein from *Bacillus subtilis* (Table 1, SEQ ID NOs: 14-15) a protein implicated in chromosome replication. No other significant similarity was found with any other protein in publicly accessible databases. The degree of relatedness of the identified ORF to the *B. subtilis* Dnal protein shows 41% identity and 63% similarity (Table 1, SEQ ID NOs: 14-15).”

3. Please replace the last paragraph (from line 15 on page 44 to line 8 on page 45) with the following paragraph:

“Using methodology described in detail in Example 1, a *S. aureus* polypeptide that specifically bound the P77 phage ORF 104 protein was isolated. The sequence of a tryptic peptide of the *S. aureus* polypeptide, GHVPENVTNDNR (SEQ ID NO: [10] 19), was used to BLAST search the *S. aureus* nucleotide sequence in the University of Oklahoma *S. aureus* genomic database at <http://www.genome.ou.edu/staph.html>. One sequence contig of 4850 nucleotides in length (Contig 981), when converted into amino acid sequence, contained within it the similar amino acid sequence GHVPELYVDNNR (SEQ ID NO: 11; Fig. 5). This tentative identification of the candidate protein was then confirmed upon *in silico* tryptic digestion of the open reading frame found in the contig (Fig. 5). The obtained PSD/CID spectra for tryptic peptides with monoisotopic MH⁺ masses of 1351.8, 1412.7, and 1617.8”